

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
 - (ii) TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
 - (iii) NUMBER OF SEQUENCES: 107
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
 - (B) STREET: 1007 MARKET STREET
 - (C) CITY: WILMINGTON
 - (D) STATE: DELAWARE
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 19898
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: FLOPPY DISK
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: MICROSOFT WORD VERSION 2.0C
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BARBARA C. SIEGELL
 - (B) REGISTRATION NUMBER: 30,684
 - (C) REFERENCE/DOCKET NUMBER: BB-1037-C
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 302-992-4931
 - (B) TELEFAX: 302-773-0164
 - (C) TELEX: 835420

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCT GAA ATT GTT GTC TCC AAA TTT GGC GGT ACC AGC GTA GCT GAT	48
Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp	
1 5 10 15	
TTT GAC GCC ATG AAC CGC AGC GCT GAT ATT GTG CTT TCT GAT GCC AAC	96
Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn	
20 25 30	
GTG CGT TTA GTT GTC CTC TCG GCT TCT GCT GGT ATC ACT AAT CTG CTG	144
Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu	
35 40 45	
GTC GCT TTA GCT GAA GGA CTG GAA CCT GGC GAG CGA TTC GAA AAA CTC	192
Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu	
50 55 60	
GAC GCT ATC CGC AAC ATC CAG TTT GCC ATT CTG GAA CGT CTG CGT TAC	240
Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr	
65 70 75 80	
CCG AAC GTT ATC CGT GAA GAG ATT GAA CGT CTG CTG GAG AAC ATT ACT	288
Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr	
85 90 95	
GTT CTG GCA GAA GCG GCG GCG CTG GCA ACG TCT CCG GCG CTG ACA GAT	336
Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp	
100 105 110	
GAG CTG GTC AGC CAC GGC GAG CTG ATG TCG ACC CTG CTG TTT GTT GAG	384
Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu	
115 120 125	
ATC CTG CGC GAA CGC GAT GTT CAG GCA CAG TGG TTT GAT GTA CGT AAA	432
Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys	
130 135 140	
GTG ATG CGT ACC AAC GAC CGA TTT GGT CGT GCA GAG CCA GAT ATA GCC	480
Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala	
145 150 155 160	
GCG CTG GCG GAA CTG GCC GCG CTG CAG CTG CTC CCA CGT CTC AAT GAA	528
Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu	

165										170										175										
GGC	TTA	GTG	ATC	ACC	CAG	GGA	TTT	ATC	GGT	AGC	GAA	AAT	AAA	GGT	CGT	576														
Gly	Leu	Val	Ile	Thr	Gln	Gly	Phe	Ile	Gly	Ser	Glu	Asn	Lys	Gly	Arg															
180										185						190														
ACA	ACG	ACG	CTT	GGC	CGT	GGA	GGC	AGC	GAT	TAT	ACG	GCA	GCC	TTG	CTG	624														
Thr	Thr	Thr	Leu	Gly	Arg	Gly	Gly	Ser	Asp	Tyr	Thr	Ala	Ala	Leu	Leu															
195										200						205														
GCG	GAG	GCT	TTA	CAC	GCA	TCT	CGT	GTT	GAT	ATC	TGG	ACC	GAC	GTC	CCG	672														
Ala	Glu	Ala	Leu	His	Ala	Ser	Arg	Val	Asp	Ile	Trp	Thr	Asp	Val	Pro															
210										215						220														
GGC	ATC	TAC	ACC	ACC	GAT	CCA	CGC	GTA	GTT	TCC	GCA	GCA	AAA	CGC	ATT	720														
Gly	Ile	Tyr	Thr	Thr	Asp	Pro	Arg	Val	Val	Ser	Ala	Ala	Lys	Arg	Ile															
225										230						235														
GAT	GAA	ATC	GCG	TTT	GCC	GAA	GCG	GCA	GAG	ATG	GCA	ACT	TTT	GGT	GCA	768														
Asp	Glu	Ile	Ala	Phe	Ala	Glu	Ala	Ala	Glu	Met	Ala	Thr	Phe	Gly	Ala															
245										250						255														
AAA	GTA	CTG	CAT	CCG	GCA	ACG	TTG	CTA	CCC	GCA	GTA	CGC	AGC	GAT	ATC	816														
Lys	Val	Leu	His	Pro	Ala	Thr	Leu	Leu	Pro	Ala	Val	Arg	Ser	Asp	Ile															
260										265						270														
CCG	GTC	TTT	GTC	GGC	TCC	AGC	AAA	GAC	CCA	CGC	GCA	GGT	GGT	ACG	CTG	864														
Pro	Val	Phe	Val	Gly	Ser	Ser	Lys	Asp	Pro	Arg	Ala	Gly	Gly	Thr	Leu															
275										280						285														
GTG	TGC	AAT	AAA	ACT	GAA	AAT	CCG	CCG	CTG	TTC	CGC	GCT	CTG	GCG	CTT	912														
Val	Cys	Asn	Lys	Thr	Glu	Asn	Pro	Pro	Leu	Phe	Arg	Ala	Leu	Ala	Leu															
290										295						300														
CGT	CGC	AAT	CAG	ACT	CTG	CTC	ACT	TTG	CAC	AGC	CTG	AAT	ATG	CTG	CAT	960														
Arg	Arg	Asn	Gln	Thr	Leu	Leu	Thr	Leu	His	Ser	Leu	Asn	Met	Leu	His															
305										310						315														
TCT	CGC	GGT	TTC	CTC	GCG	GAA	GTT	TTC	GGC	ATC	CTC	GCG	CGG	CAT	AAT	1008														
Ser	Arg	Gly	Phe	Leu	Ala	Glu	Val	Phe	Gly	Ile	Leu	Ala	Arg	His	Asn															
325										330						335														
ATT	TCG	GTA	GAC	TTA	ATC	ACC	ACG	TCA	GAA	GTG	AGC	GTG	GCA	TTA	ACC	1056														
Ile	Ser	Val	Asp	Leu	Ile	Thr	Thr	Ser	Glu	Val	Ser	Val	Ala	Leu	Thr															
340										345						350														
CTT	GAT	ACC	ACC	GGT	TCA	ACC	TCC	ACT	GGC	GAT	ACG	TTG	CTG	ACG	CAA	1104														
Leu	Asp	Thr	Thr	Gly	Ser	Thr	Ser	Thr	Gly	Asp	Thr	Leu	Leu	Thr	Gln															
355										360						365														
TCT	CTG	CTG	ATG	GAG	CTT	TCC	GCA	CTG	TGT	CGG	GTG	GAG	GTG	GAA	GAA	1152														
Ser	Leu	Leu	Met	Glu	Leu	Ser	Ala	Leu	Cys	Arg	Val	Glu	Val	Glu	Glu															
370										375						380														
GGT	CTG	GCG	CTG	GTC	GCG	TTG	ATT	GGC	AAT	GAC	CTG	TCA	AAA	GCC	TGC	1200														
Gly	Leu	Ala	Leu	Val	Ala	Leu	Ile	Gly	Asn	Asp	Leu	Ser	Lys	Ala	Cys															
385										390						395														
																400														

GCC GTT GGC AAA GAG GTA TTC GGC GTA CTG GAA CCG TTC AAC ATT CGC 1248
 Ala Val Gly Lys Glu Val Phe Gly Val Leu Glu Pro Phe Asn Ile Arg
 405 410 415

ATG ATT TGT TAT GGC GCA TCC AGC CAT AAC CTG TGC TTC CTG GTG CCC 1296
 Met Ile Cys Tyr Gly Ala Ser Ser His Asn Leu Cys Phe Leu Val Pro
 420 425 430

GGC GAA GAT GCC GAG CAG GTG GTG CAA AAA CTG CAT AGT AAT TTG TTT 1344
 Gly Glu Asp Ala Glu Gln Val Val Gln Lys Leu His Ser Asn Leu Phe
 435 440 445

GAG TAA 1350
 Glu +
 450

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCCATGGC TGAAATTGTT GTCTCCAAAT TTGGCG 36

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTACCGCCAA ATTTGGAGAC AACAAATTCA GCCATG 36

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCGGGCCAT GGCTACAGGT TTAACAGCTA AGACCGGAGT AGAGCACT 48

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATATCGAAT TCTCATTATA GAACTCCAGC TTTTTC 37

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 917 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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CC ATG GCT ACA GGT TTA ACA GCT AAG ACC GGA GTA GAG CAC TTC GGC 47
  Met Ala Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly
    1             5             10             15

ACC GTT GGA GTA GCA ATG GTT ACT CCA TTC ACG GAA TCC GGA GAC ATC 95
  Thr Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile
                20             25             30

GAT ATC GCT GCT GGC CGC GAA GTC GCG GCT TAT TTG GTT GAT AAG GGC 143
  Asp Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly
                35             40             45

TTG GAT TCT TTG GTT CTC GCG GGC ACC ACT GGT GAA TCC CCA ACG ACA 191
  Leu Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr
    50             55             60

ACC GCC GCT GAA AAA CTA GAA CTG CTC AAG GCC GTT CGT GAG GAA GTT 239
  Thr Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val
    65             70             75

GGG GAT CGG GCG AAG CTC ATC GCC GGT GTC GGA ACC AAC AAC ACG CGG 287
  Gly Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg
    80             85             90             95

ACA TCT GTG GAA CTT GCG GAA GCT GCT GCT TCT GCT GGC GCA GAC GGC 335
  Thr Ser Val Glu Leu Ala Glu Ala Ala Ser Ala Gly Ala Asp Gly
    100            105            110

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CTT	TTA	GTT	GTA	ACT	CCT	TAT	TAC	TCC	AAG	CCG	AGC	CAA	GAG	GGA	TTG	383
Leu	Leu	Val	Val	Thr	Pro	Tyr	Tyr	Ser	Lys	Pro	Ser	Gln	Glu	Gly	Leu	
			115					120				125				
CTG	GCG	CAC	TTC	GGT	GCA	ATT	GCT	GCA	GCA	ACA	GAG	GTT	CCA	ATT	TGT	431
Leu	Ala	His	Phe	Gly	Ala	Ile	Ala	Ala	Ala	Thr	Glu	Val	Pro	Ile	Cys	
			130				135				140					
CTC	TAT	GAC	ATT	CCT	GGT	CGG	TCA	GGT	ATT	CCA	ATT	GAG	TCT	GAT	ACC	479
Leu	Tyr	Asp	Ile	Pro	Gly	Arg	Ser	Gly	Ile	Pro	Ile	Glu	Ser	Asp	Thr	
	145					150					155					
ATG	AGA	CGC	CTG	AGT	GAA	TTA	CCT	ACG	ATT	TTG	GCG	GTC	AAG	GAC	GCC	527
Met	Arg	Arg	Leu	Ser	Glu	Leu	Pro	Thr	Ile	Leu	Ala	Val	Lys	Asp	Ala	
	160				165					170					175	
AAG	GGT	GAC	CTC	GTT	GCA	GCC	ACG	TCA	TTG	ATC	AAA	GAA	ACG	GGA	CTT	575
Lys	Gly	Asp	Leu	Val	Ala	Ala	Thr	Ser	Leu	Ile	Lys	Glu	Thr	Gly	Leu	
			180						185					190		
GCC	TGG	TAT	TCA	GGC	GAT	GAC	CCA	CTA	AAC	CTT	GTT	TGG	CTT	GCT	TTG	623
Ala	Trp	Tyr	Ser	Gly	Asp	Asp	Pro	Leu	Asn	Leu	Val	Trp	Leu	Ala	Leu	
			195				200						205			
GGC	GGA	TCA	GGT	TTC	ATT	TCC	GTA	ATT	GGA	CAT	GCA	GCC	CCC	ACA	GCA	671
Gly	Gly	Ser	Gly	Phe	Ile	Ser	Val	Ile	Gly	His	Ala	Ala	Pro	Thr	Ala	
			210				215					220				
TTA	CGT	GAG	TTG	TAC	ACA	AGC	TTC	GAG	GAA	GGC	GAC	CTC	GTC	CGT	GCG	719
Leu	Arg	Glu	Leu	Tyr	Thr	Ser	Phe	Glu	Glu	Gly	Asp	Leu	Val	Arg	Ala	
	225					230					235					
CGG	GAA	ATC	AAC	GCC	AAA	CTA	TCA	CCG	CTG	GTA	GCT	GCC	CAA	GGT	GCG	767
Arg	Glu	Ile	Asn	Ala	Lys	Leu	Ser	Pro	Leu	Val	Ala	Ala	Gln	Gly	Arg	
	240				245				250					255		
TTG	GGT	GGA	GTC	AGC	TTG	GCA	AAA	GCT	GCT	CTG	CGT	CTG	CAG	GGC	ATC	815
Leu	Gly	Gly	Val	Ser	Leu	Ala	Lys	Ala	Ala	Leu	Arg	Leu	Gln	Gly	Ile	
			260					265						270		
AAC	GTA	GGA	GAT	CCT	CGA	CTT	CCA	ATT	ATG	GCT	CCA	AAT	GAG	CAG	GAA	863
Asn	Val	Gly	Asp	Pro	Arg	Leu	Pro	Ile	Met	Ala	Pro	Asn	Glu	Gln	Glu	
			275				280						285			
CTT	GAG	GCT	CTC	CGA	GAA	GAC	ATG	AAA	AAA	GCT	GGA	GTT	CTA	TAA	TGAGAATTC	918
Leu	Glu	Ala	Leu	Arg	Glu	Asp	Met	Lys	Lys	Ala	Gly	Val	Leu	*		
			290				295					300				

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTCCCGTGA CCATGGGCCA TC

22

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATGGGTGGC TTCCCCACGA GGAAGACCAA CAATGACATT ACCTCCATTG CTAGCAACGG 60
TGAAGAGTA CAATG 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATGCATTGT ACTCTTCCAC CGTTGCTAGC AATGGAGGTA ATGTCATTGT TGGTCTTCCT 60
CGTGGGGAAG CCAGC 75

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATGGCTTCC TCAATGATCT CCTCCCAGC TGTTACCACC GTCAACCGTG CCGGTGCCGG 60
CATGGTTGCT CCATTACCG GCCTCAAAG 90

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATGCTTTTG AGGCCGGTGA ATGGAGCAAC CATGCCGGCA CCGGCACGGT TGACGGTGGT 60
AACAGCTGGG GAGGAGATCA TTGAGGAAGC 90

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGTTTGCT GTAATAGGTA CCA 23

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTTGTAC CTATTACAGC AAACCGGCAT G 31

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTTCCTCAA TGATCTCCTC CCCAGCT 27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATTGTACTC TTCCACCGTT GCTAGCAA 28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
70"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTGACTCGCT GCGCTCGGTC 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..24
(D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
71"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TATTTCTCC TTACGCATCT GTGC 24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
78"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCATCGATA GGCGACCACA CCCGTCC

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
79"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AATATCGATG CCACGATGCG TCCGGCG

27

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
81"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATGGAGGAG AAGATGAAGG CGATGGAAGA GAAGATGAAG GCGTGATAGG TACCG 55

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
80"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTCGGTAC CTATCAGCC TTCATCTTCT CTTCCATCGC CTTCATCTTC TCCTC 55

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..14
- (D) OTHER INFORMATION: /label= name
/note= "base gene
[(SSP5)2]"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
84"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATGGAGGAG AAGATGAAGG C

21

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
85"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCGCCTTCA TCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
82"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATGGAGGAG AAGCTGAAGG C

21

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..21
 - (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
83"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATCGCCTTCA GCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Glu Lys Leu Lys Ala

1

5

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Glu Glu Lys Met Lys Ala

1

5

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 base pairs
 - (B) TYPE: nucleic acid

```

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: C15

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..151
(D) OTHER INFORMATION: /function= "synthetic
                        storage protein"
                        /product= "protein"
                        /gene= "ssp"
                        /standard_name=
                        "5.7.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG      46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met
    1             5             10             15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG    94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
    20             25             30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG   142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
    35             40             45

AAG GCG TGATAGGTAC CG                                           160
Lys Ala
    50

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
  1             5             10             15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Lys
    20             25             30

```

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
 35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: C20
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..151
 - (D) OTHER INFORMATION: /function= "synthetic storage protein"
 /product= "protein"
 /gene= "snp"
 /standard_name= "5.7.7.7.7.5"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

C	ATG	GAG	GAG	AAG	ATG	AAG	GCG	ATG	GAG	GAG	AAG	CTG	AAG	GCG	ATG	46
	Met	Glu	Glu	Lys	Met	Lys	Ala	Met	Glu	Glu	Lys	Leu	Lys	Ala	Met	
	1				5						10				15	
GAG	GAG	AAG	CTG	AAG	GCG	ATG	GAG	GAG	AAG	CTG	AAG	GCG	ATG	GAG	GAG	94
Glu	Glu	Lys	Leu	Lys	Ala	Met	Glu	Glu	Lys	Leu	Lys	Ala	Met	Glu	Glu	
			20						25					30		
AAG	CTG	AAG	GCG	ATG	GAG	GAG	AAG	CTG	AAG	GCG	ATG	GAA	GAG	AAG	ATG	142
Lys	Leu	Lys	Ala	Met	Glu	Glu	Lys	Leu	Lys	Ala	Met	Glu	Glu	Lys	Met	
			35				40					45				
AAG	GCG	TGATAGGTAC	CG													160
Lys	Ala															
			50													

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1 5 10 15
 Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
 20 25 30
 Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
 35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: C30
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..130
 - (D) OTHER INFORMATION: /function= "synthetic
 storage protein"
 /product= "protein"
 /gene= "ssp"
 /standard_name=
 "5.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG 46
 Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met
 1 5 10 15
 GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 94
 Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
 20 25 30
 AAG CTG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CG 139
 Lys Leu Lys Ala Met Glu Glu Lys Met Lys Ala
 35 40

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1              5              10              15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
              20              25              30

Leu Lys Ala Met Glu Glu Lys Met Lys Ala
 35              40

```

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (B) STRAIN: E. coli
 (G) CELL TYPE: DH5 alpha

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: D16

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..88
 (D) OTHER INFORMATION: /function= "synthetic
 storage protein"
 /product= "protein"
 /gene= "ssp"
 /standard_name=
 "5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG   46
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
 1              5              10              15

GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC  95
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
              20              25

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
  1             5             10             15
Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
          20             25
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: D20

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..109
- (D) OTHER INFORMATION: /function= "synthetic
storage protein"
/product= "protein"
/gene= "ssp"
/standard_name=
"5.5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG      46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
    1             5             10             15

GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG GAA GAG    94
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu
          20             25             30

AAG ATG AAG GCG TGATAGGTAC CG                                     118
Lys Met Lys Ala
          35
```

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
 1             5             10             15
Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys
      20             25             30
Met Lys Ala
      35

```

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: D33

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..88
 - (D) OTHER INFORMATION: /function= "synthetic
storage protein"
/product= "protein"
/gene= "ssp"
/standard_name=
"5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG   46
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
 1             5             10             15
GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC   95
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
      20             25

```

CG

97

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
 1              5              10              15
Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
                20              25

```

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..21
 - (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
86"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

GATGGAGGAG AAGCTGAAGA A
                                21

```

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..21
 - (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
87"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATCTTCTTCA GCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
88"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATGGAGGAG AAGCTGAAGT G

21

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
89"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATCCACTTCA GCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /product= "synthetic
 oligonucleotide"
 /standard_name= "SM
 90"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATGGAGGAG AAGATGAAGA A 21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /product= "synthetic
 oligonucleotide"
 /standard_name= "SM
 91"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTTCTTCA TCTTCTCCTC C 21

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /product= "synthetic
 oligonucleotide"
 /standard_name= "SM
 92"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GATGGAGGAG AAGATGAAGT G 21

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..21
 - (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
93"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATCCACTTCA TCTTCTCCTC C

21

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Glu Glu Lys Leu Lys Lys

1

5

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Glu Glu Lys Leu Lys Trp

1

5

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Glu Glu Lys Met Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Glu Lys Met Lys Trp
1 5

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha
- (vii) IMMEDIATE SOURCE:
(B) CLONE: 82-4
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..151
(D) OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
"7.7.7.7.7.5"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG 46
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
1 5 10 15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG 94
 Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
 20 25 30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142
 Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
 35 40 45

AAG GCG TGATAGGTAC CG 160
 Lys Ala
 50

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1 5 10 15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
 20 25 30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
 35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (B) STRAIN: E. coli
 (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 84-H3

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..88
 (D) OTHER INFORMATION: /function= "synthetic
 storage protein
 /product= "protein"

/gene= "ssp"
 /standard_name=
 "5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46
 Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
 1 5 10 15

GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95
 Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
 20 25

CG 97

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
 1 5 10 15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
 (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 86-H23

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 2..88
 (D) OTHER INFORMATION: /function= "synthetic
 storage protein
 /product= "protein"
 /gene= "ssp"

/standard_name=
"5.8.8.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG AAG ATG   46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met
    1             5             10             15

GAG GAG AAG CTG AAG AAG ATG CAA GAG AAG ATG AAG GCG TGATAGGTAC   95
  Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala
                20             25

CG                                                                97

```

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met Glu
  1             5             10             15

Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala
    20             25

```

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (B) STRAIN: E. coli
 (G) CELL TYPE: DH5 alpha

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: 88-2

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..103
 (D) OTHER INFORMATION: /function= "synthetic
 storage protein
 /product= "protein"
 /gene= "ssp"
 /standard_name=
 "5.9.9.9.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

C ATG GAG GAG AAG ATG AAG GCG AAG AAG CTG AAG TGG ATG GAG GAG 46
 Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu
 1 5 10 15

AAG CTG AAG TGG ATG GAG GAG AAG CTG AAG TGG ATG GAA GAG AAG ATG 94
 Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met
 20 25 30

AAG GCG TGATAGGTAC CG 112
 Lys Ala

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu Lys
 1 5 10 15

Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys
 20 25 30

Ala

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (B) STRAIN: E. coli
 (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 90-H8

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..109
 (D) OTHER INFORMATION: /function= "synthetic
 storage protein
 /product= "protein"
 /gene= "ssp"

/standard_name=
"5.10.10.10.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG AAG ATG   46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met
    1             5             10             15

GAG GAG AAG ATG AAG AAG ATG GAG GAG AAG ATG AAG AAG ATG GAA GAG 94
Glu Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Glu
    20             25             30

AAG ATG AAG GCG TGATAGGTAC CG                               118
Lys Met Lys Ala
    35

```

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met Glu
  1             5             10             15

Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Lys
    20             25             30

Met Lys Ala
    35

```

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
- (B) STRAIN: E. coli
 - (G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 92-2

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 2..88

(D) OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
"5.11.11.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

C	ATG	GAG	GAG	AAG	ATG	AAG	GCG	ATG	GAG	GAG	AAG	ATG	AAG	TGG	ATG	46
	Met	Glu	Glu	Lys	Met	Lys	Ala	Met	Glu	Glu	Lys	Met	Lys	Trp	Met	
	1				5				10					15		
GAG	GAG	AAG	ATG	AAG	TGG	ATG	GAA	GAG	AAG	ATG	AAG	GCG	TGATAGGTAC			95
Glu	Glu	Lys	Met	Lys	Trp	Met	Glu	Glu	Lys	Met	Lys	Ala				
				20					25							
CG																97

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met	Glu	Glu	Lys	Met	Lys	Ala	Met	Glu	Glu	Lys	Met	Lys	Trp	Met	Glu
1				5				10					15		
Glu	Lys	Met	Lys	Trp	Met	Glu	Glu	Lys	Met	Lys	Ala				
				20				25							

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..84
 (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
96"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATGGAGGAA AAGATGAAGG CGATGGAGGA GAAATGAAA GCTATGGAGG AAAAGATGAA 60

AGCGATGGAG GAGAAAATGA AGGC

84

(2) INFORMATION FOR SEQ ID NO:66:

- ```
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..84
(D) OTHER INFORMATION: /product= "synthetic
 oligonucleotide"
 /standard_name= "SM
 97"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
```

ATCGCCTTCA TTTCTCCTC CATCGCTTC ATCTTTTCCT CCATAGCTTT CATTTTCTCC 60  
TCCATCGCCT TCATCTTTTC CTCC 84

(2) INFORMATION FOR SEQ ID NO:67:

- ```
(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 28 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS: unknown
  (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
  (A) NAME/KEY: Protein
  (B) LOCATION: 1..28
  (D) OTHER INFORMATION: /label= name
                        /note= "(SSP 5)4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
```

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
1 5 10 15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
20 25

(2) INFORMATION FOR SEO ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
  (A) NAME/KEY: misc_feature
  (B) LOCATION: 1..84
  (D) OTHER INFORMATION: /product= "synthetic
                        oligonucleotide"
                        /standard_name= "SM
                        98"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GATGGAGGAA AAGCTGAAAG CGATGGAGGA GAAACTCAAG GCTATGGAAG AAAAGCTTAA 60
AGCGATGGAG GAGAAACTGA AGGC                                         84

(2) INFORMATION FOR SEQ ID NO:69:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 84 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION: 1..84
    (D) OTHER INFORMATION: /product= "synthetic
                          oligonucleotide"
                          /standard_name= "SM
                          99"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATCGCCTTCA GTTTCCTCTC CTACGCTTTA AGCTTTTCTT CCATAGCCTT GAGTTTCTCC 60
TCCATCGCTT TCAGCTTTTC CTCC                                         84

(2) INFORMATION FOR SEQ ID NO:70:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 28 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: unknown
    (D) TOPOLOGY: unknown

  (ii) MOLECULE TYPE: protein

  (ix) FEATURE:
    (A) NAME/KEY: Protein
    (B) LOCATION: 1..28
    (D) OTHER INFORMATION: /label= name
                          /note= "(SSP 7)4"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1 5 10 15
 Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /product= "synthetic
 oligonucleotide"
 /standard_name= "SM
 100"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GATGGAGGAA AAGCTTAAGA AGATGGAAGA AAAGCTGAAA TGGATGGAGG AGAAACTCAA 60
 AAAGATGGAG GAAAAGCTTA AATG 84

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /product= "synthetic
 oligonucleotide"
 /standard_name= "SM
 101"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATCCATTAA GCTTTTCCTC TACTTTTGTG AGTTTCCTCT CCATCCATTT CAGCTTTTCT 60
 TCCATCTTCT TAAGCTTTTC CTCC 84

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
Met Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu
 1             5             10             15
Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp
                20             25
```

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 (B) STRAIN: E. coli
 (G) CELL TYPE: DH5 alpha
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: 2-9
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..235
 (D) OTHER INFORMATION: /function= "synthetic
 storage protein
 /product= "protein"
 /gene= "ssp"
 /standard_name=
 "7.7.7.7.7.8.9.8.9.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG      46
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
 1             5             10             15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG      94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                20             25             30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAA AAG CTT      142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu
                35             40             45

AAG AAG ATG GAA GAA AAG CTG AAA TGG ATG GAG GAG AAA CTC AAA AAG      190
Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys
                50             55             60
```


/standard_name=
"5.5.5.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

C  ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG   46
   Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
   1             5             10             15

GAG GAG AAG ATG AAG GCG ATG GAG GAA AAG CTG AAA GCG ATG GAG GAG   94
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                20             25             30

AAA CTC AAG GCT ATG GAA GAA AAG CTT AAA GCG ATG GAG GAG AAA CTG 142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu
                35             40             45

AAG GCC ATG GAA GAG AAG ATG AAG GCG TGATAG                       179
Lys Ala Met Glu Glu Lys Met Lys Ala
                50             55

```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
   1             5             10             15

Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
                20             25             30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys
                35             40             45

Ala Met Glu Glu Lys Met Lys Ala
                50             55

```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: E. coli
- (G) CELL TYPE: DH5 alpha

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 3..173
 (D) OTHER INFORMATION: /function= "synthetic
 storage protein"
 /product= "protein"
 /gene= "ssp"
 /standard_name=
 "SSP-3-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

CC ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG   47
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
  1                      5                      10                      15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG   95
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                      20                      25                      30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAA AAG ATG  143
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
                      35                      40                      45

AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CGAATTC           187
Lys Ala Met Glu Glu Lys Met Lys Ala
                      50                      55

```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
  1                      5                      10                      15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
                      20                      25                      30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
                      35                      40                      45

Ala Met Glu Glu Lys Met Lys Ala
                      50                      55

```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
107"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CATGGAGGAG AAGATGAAAA AGCTCGAAGA GAAGATGAAG GTCATGAAGT GATAGGTACC 60

G

61

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: /product= "synthetic
ligonucleotide"
/standard_name= "SM
106"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATTCGGTAC CTATCACTTC ATGACCTTCA TCTTCTCTTC GAGCTTTTTC ATCTTCTCCT 60

C

61

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /label= name
/note= "pSK34 base
gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /product= "synthetic
 oligonucleotide"
 /standard_name= "SM
 110"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCTGGAAGAA AAGATGAAGG CTATGGAGGA CAAGATGAAA TGGCTTGAGG AAAAGATGAA 60
 GAA 63

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /product= "synthetic
 oligonucleotide"
 /standard_name= "SM
 111"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

AGCTTCTTCA TCTTTTCCTC AAGCCATTTC ATCTTGTCTT CCATAGCCTT CATCTTTTCT 60
 TCC 63

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu
 1              5              10              15
Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu Glu Glu Lys
              20              25              30
Met Lys Val Met Lys
              35

```

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu
 1              5              10              15
Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu Glu Glu Lys
              20              25              30
Met Lys Val Met Lys
              35

```

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..62
 - (C) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
112"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCTCGAAGAA AGATGAAGGC AATGAAGAC AAAATGAAGT GGCTTGAGGA GAAAATGAAG 60

AA

62

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
113"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGCTTCTTCA TTTTCTCCTC AAGCCACTTC ATTTGTCTT CCATTGCCTT CATCTTTCTT 60

CG

62

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met	Glu	Glu	Lys	Met	Lys	Lys	Leu	Lys	Glu	Glu	Met	Ala	Lys	Met	Lys
1				5				10					15		

Asp	Glu	Met	Trp	Lys	Leu	Lys	Glu	Glu	Met	Lys	Lys	Leu	Glu	Glu	Lys
			20				25					30			

Met	Lys	Val	Met	Lys
			35	

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
114"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTCAAGGAG GAAATGGCTA AGATGAAAGA CGAAATCTGG AAAGTAAAG AGGAAATGAA 60
GAA 63

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
115"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AGCTTCTTCA TTTCTCTTT CAGTTTCAC ATTTCGTCTT TCATCTTAGC CATTTCTCC 60
TTG 63

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met	Glu	Glu	Lys	Met	Lys	Lys	Leu	Lys	Glu	Glu	Met	Ala	Lys	Met	Lys
1				5				10					15		
Asp	Glu	Met	Trp	Lys	Leu	Lys	Glu	Glu	Met	Lys	Lys	Leu	Glu	Glu	Lys
			20				25					30			
Met	Lys	Val	Met	Glu	Glu	Lys	Met	Lys	Lys	Leu	Glu	Glu	Lys	Met	Lys

35	40	45
Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu		
50	55	60
Glu Glu Lys Met Lys Val Met Glu Glu Lys Met Lys Lys Leu Glu Glu		
65	70	75
Lys Met Lys Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met		
	85	90
		95
Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys		
100	105	

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

GGATCCCCCG GGCTGCAGGA ATTCTACGTA CCATATAGTA AGACTTTGTA TATAAGACGT 60
CACCTCTTAC GTGTCAGGTT ATATGTGACA TGTGCAGTGA CGTTGTACCA TACTAGTAAGA 120
CTTTGTATAT AAGACGTCAC CTCTTACGTG CATGGTTATA TGTGACATGT GCAGTGACGT 180
TAACCGCACC CTCCTTCCCG TCGTTTCCCA TCTCTTCCTC CTTTAGAGCT ACCACTATAT 240
AAATCAGGGC TCATTTTCTC GCTCCTCACA GGCTCATCAG CACCCCGGCA GTGCCACCCC 300
GACTCCCTGC ACCTGCCATG GGTACGCTAG CCCGGGAGAT CTGACAAAGC AGCATTAGTC 360
CGTTGATCGG TGGAAGACCA CTCGTCAGTG TTGAGTTGAA TGTTTGATCA ATAAAAATACG 420
GCAATGCTGT AAGGGTTGTT TTTTATGCCA TTGATAATAC ACTGTACTGT TCAGTTGTTG 480
AACTCTATTT CTTAGCCATG CCAGTGCTTT TCTTATTTTG AATAACATTA CAGCAAAAAA 540
TTGAAGAGCA AAAAAANNNN NCCCCGAACA GAGTGCTTTG GGTCCCAAGC TTCTTTAGAC 600
TGTGTTCCGC GTTCCCCTTA AATTCTCTCC CTATATCTCA CTCACTTGTC ACATCAGCGT 660
TCTCTTTCCC CTATATCTCC ACGCTCTACA GCAGTTCCAC CTATATCAAA CCTCTATACC 720
CCACCACAAC AATATTATAT ACTTTCATCT TCACCTAACT CATGTACCTT CCAATTTTTT 780
TCTACTAATA ATTATTTACG TGCACAGAAA CTTAGGCAAG GGAGAGAGAG AGCGGTACC 839

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(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTAGAAGCCT CGGCAACGTC AGCAACGGCG GAAGAATCCG GTG 43

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CATGCACCGG ATTCTTCCGC CGTTGCTGAC GTTGCCGAGG CTT 43

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GATCCCATGG CGCCCCCTTAA GTCCACCGCC AGCCTCCCCG TCGCCGCCG CTCCT 55

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTAGAGGAGC GCGGGGCGAC GGGGAGGCTG GCGGTGGACT TAAGGGGCGC CATGG 55

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CATGGCGCCC ACCGTGATGA TGGCCTCGTC GGCCACCGCC GTCGCTCCGT TCCAGGGGC
59

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TTAAGCCCCCT GGAACGGAGC GACGGCGGTG GCCGACGAGG CCATCATCAC GGTGGGCGC
59

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCGCCACCG TGATGA

16

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CACCGATTTC TTCCGC

16

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

5 GTAAGATTGG TAAAGTCCAG CAAGAAAATG AGATAAAAGA GAAGCCTGAA ATGACGAAAA 60
AATCAGGTGT TTTGATTCTT GGTGCTGGAC GTGTGTNTCG CCCAGCTGCT GATTTCCTAG 120
CTTCAGTTAG AACCATTTCG TCACAGCAAT GGTACAAAAC ATATTTCGGA GCAGACTCTG 180
10 AAGAGAAAAA AGATGTTTAT GTGATTGTCT CGTCTCTGTA TCTTAAAGGAT GCCAAAGAGA 240
CGGTTGAAGG TATTTCAGAT GTAGAAGCAG TTCGGCTAGA TGTATCTGAT AGTGAAAGTC 300
15 TCCTTAAGTA TGTTTCTCAG GTTGATGTTG TCCTAAGTTT ATTACCTGCA AGTTGTCATG 360
CTTGTGTAG CA 372

(2) INFORMATION FOR SEQ ID NO:103:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic) /

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

25 GGAAGCACAC TGCAGCTCTT TTGGAATTCG GGGACATCAA GAATGGACAA ACAACAACCG 60
CTATGGCCAA GACTGTTGGG ATCCCTGCAG CCATTGGAGC TCTGCTGTTA ATTGAAGACA 120
30 AGATCAAGAC AAGAGGAGTC TTAAGGCCTC TCGAAGCAGA GGTGTATTG CCAGCTTGG 180
ATATATTGCA AGCATATGCT ATAAAGCTGA TGGAGAAGGC AGAATGATCA AAGAACTCTG 240
TATATTGTTT CTNCTATAA CTTGGAGTTG GAGACAAAGC TGAAGGAGNC AGNGCCATTA 300
35 GACCAGCAAA AAAAGGAGGA GGA 323

(2) INFORMATION FOR SEQ ID NO:104:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

5 Lys Ile Gly Lys Val Gln Gln Glu Asn Glu Ile Lys Glu Lys Pro Glu
 1 5 10 15
 Met Thr Lys Lys Ser Gly Val Leu Ile Leu Gly Ala Gly Arg Val Xaa
 20 25 30
 10 Arg Pro Ala Ala Asp Phe Leu Ala Ser Val Arg Thr Ile Ser Ser Gln
 35 40 45
 Gln Trp Tyr Lys Thr Tyr Phe Gly Ala Asp Ser Glu Glu Lys Thr Asp
 50 55 60
 15 Val His Val Ile Val Ala Ser Leu Tyr Leu Lys Asp Ala Lys Glu Thr
 65 70 75 80
 Val Glu Gly Ile Ser Asp Val Glu Ala Val Arg Leu Asp Val Ser Asp
 85 90 95
 20 Ser Glu Ser Leu Leu Lys Tyr Val Ser Gln Val Asp Val Val Leu Ser
 100 105 110
 Leu Leu Pro Ala Ser Cys His Ala Cys Cys Ser
 115 120

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

35 Lys His Thr Ala Thr Leu Leu Glu Phe Gly Asp Ile Lys Asn Gly Gln
 1 5 10 15
 Thr Thr Thr Ala Met Ala Lys Thr Val Gly Ile Pro Ala Ala Ile Gly
 20 25 30
 40 Ala Leu Leu Leu Ile Glu Asp Lys Ile Lys Thr Arg Gly Val Leu Arg
 35 40 45
 Pro Leu Glu Ala Glu Val Tyr Leu Pro Ala Leu Asp Ile Leu Gln Ala
 50 55 60
 45 Tyr Gly Ile Lys Leu Met Glu Lys Ala Glu
 65 70

50 (2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

5

ATTCCCCATG GTTTCGCCGA CGAAT

25

(2) INFORMATION FOR SEQ ID NO:107:

10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

15

CTCTCGGTAC CTAGTACCTA CTGATCAAC

29